

D3

--(SEQ ID NO 4, 29 nucleotides, Tm = 86°C), and--

Page 22, delete the paragraph on line 33 and insert the following therefor:

D4

--(SEQ ID NO 5, 35 nucleotides, Tm = 81°C).--

Page 23, delete the paragraph spanning lines 5-6 and insert the following

therefor:

D5

-- - ribozyme 1: CUCCAGCUGA UGAGUCCGUG AGGACGAAAC CUUUGG

(SEQ ID NO 6)--

Page 23, delete the paragraph spanning lines 8-9 and insert the following

therefor:

D6

-- - ribozyme 2: CUGGAAUCUG AUGAGUCCGU GAGGACGAAA UUUUCUUC

(SEQ ID NO 7)--

IN THE CLAIMS

Amend the claims as follows:

Cancel claim 16, without prejudice

17. (Amended) The method of claim 39, wherein the primers consist of 25 to 40 nucleotides.

18. (Amended) The method of claim 39, further comprising, labeling said PCR products, denaturing said labeled PCR products, and contacting the denatured labeled PCR products with a nucleotide sequence complementary to a fusion partner nucleotide sequence.

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F1

21. (Amended) The method of claim 39, wherein one of the primers consists of a sequence containing a cassette of 40 to 60 nucleotides and 10 to 20 T nucleotides, and the second primer is a random repeat of nucleotides.

22. (Amended) The method of claim 39, wherein said part of the genome adjacent to the target gene is a fusion partner.

23. (Amended) The method of claim 22, comprising:

- a) subjecting the patient's genome DNA or RNA to the action of a compound capable of cleaving or specifically inhibiting the DNA or RNA of the target gene, the fusion of which is to be detected,
- b) performing said PCR,
- c) reacting the PCR products thus obtained with two probes specific for each target gene, one being upstream, and the other one being downstream, and with probes complementary to known fusion partners,

a positive detection on the upstream probe and a negative detection on the downstream probe, corresponding to a rearrangement of the target genes, and a negative detection for the known partner genes corresponding to the absence of fusion with a known fusion partner, or alternatively,

d) reacting the PCR products with a plurality of probes bonded to a miniaturized support, and detecting hybridization of the probes with the PCR products, if any.

25. (Amended) The method of claim 24, comprising

- a) the RT synthesis of a cDNA pool from the patient's RNA, using primers with a cassette,

b) a PCR amplification using a first primer located on the MLL exon 5, as specific sense primer, the 3' primer being complementary to the oligonucleotide cassette used in the RT step.

D10 SUB 29. (Amended) The method of claim 39, wherein said pathology is leukemia.

E1 30. (Amended) The method of claim 39, wherein said pathology concerns solid tumors.

D11 SUB 32. (Amended) A kit for the detection and identification method according to claim 39, comprising primers specific for the target genes and reagents for carrying out the anchored PCR and detection step.

D12 SUB 34. (Amended) A kit according to claim 32, further comprising probes complementary to the target genes and probes complementary to known fusion partners.

Add the following claim:

D13 SUB 39. (New) An *in vitro* diagnostic method for detecting and identifying DNA sequences involved in pathologies associated with rearrangements of a target gene, wherein a patient DNA or cDNA is subjected to an anchored PCR, *in vitro*, comprising:

a. amplifying the DNA or cDNA by one or more PCR, with one pair of primers, one of the primers being complementary to the nucleotide sequence of the target gene, the other primer being a complementary anchored primer, wherein all the DNA sequences adjacent to the target gene are amplified,

b. obtaining PCR products,

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